

AMENDMENT OF THE CLAIMS

Please amend the claims as follows. Language to be added is shown with an underline, and language to be deleted is shown with a strikethrough. This listing of claims will replace all prior versions and listings of claims in the application.

1. (Currently amended) A method for determining whether a human immunodeficiency virus type 1 virus (HIV-1) has an increased likelihood of having a reduced susceptibility to treatment with amprenavir, comprising:

detecting the presence or absence of a mutation in a protease associated with reduced susceptibility to treatment with amprenavir at amino acid position 11, 34, 47, 50, 76, 83, 91 or 95 of an amino acid sequence of said protease, wherein the mutation at position 11 is isoleucine (I) or leucine (L), the mutation at amino acid position 34 is glutamine (Q), the mutation at position 76 is valine (V), the mutation at position 83 is aspartic acid (D), the mutation at position 91 is alanine (A), valine (V), or serine (S), and the mutation at position 95 is phenylalanine (F), with the proviso that said mutation is not I47V or I50V, and

determining whether the HIV-1 has an increased likelihood of having a reduced susceptibility to treatment with amprenavir, wherein the presence of said mutation indicates that the HIV-1 has an increased likelihood of having a reduced susceptibility to treatment with amprenavir, and wherein the level of susceptibility, mutations, and amino acid position number are compared to the protease sequence of the NL4-3 reference strain.

2.-12. (Canceled)

13. (Currently amended) The method of claim 1 ~~12~~, wherein the amino acid at position 11 of said protease is detected I or L.

14.-20. (Canceled)

21. (Currently amended) The method of claim 1 ~~12~~, wherein the amino acid at position 76 of said protease is detected ~~V~~.

22.-23. (Canceled)

24. (Currently amended) The method of claim 1 ~~12~~, wherein the amino acid at position 91 of said protease is detected ~~A or V~~.

25. (Currently amended) The method of claim 1 ~~12~~, wherein the amino acid at position 95 of said protease is detected ~~F~~.

26.-30. (Canceled)

31. (Currently amended) The method of claim 1, wherein the amino acid at position 83 of said protease is detected ~~D~~.

32.-40. (Canceled)

41. (Currently amended) The method of claim 1-40, wherein the amino acid at position 91 of said protease is detected ~~S~~.

42. (Currently amended) The method of claim 1, wherein the method comprises detecting the presence or absence of a mutation associated with reduced susceptibility to treatment with amprenavir ~~said protease inhibitor~~ at each one of at least 2, 3, 4, 5, or 6, ~~7~~ ~~or~~ 8 of the amino acid positions.

43. (Currently amended) The method of claim 1, further comprising detecting the presence or absence of a mutation in at least one amino acid position selected from the group consisting of position 32, 33, 43, 46, 48, 54, 58, 71, ~~79~~, 82, and 84, wherein the mutation at position 32 is isoleucine (I); the mutation at position 33 is phenylalanine (F); the mutation at position 43 is threonine (T); the mutation at position 46 is isoleucine (I), leucine (L), or valine (V); the mutation at position 48 is methionine (M), serine (S), or

valine (V); the mutation at position 54 is alanine (A), serine (S), threonine (T), leucine (L), valine (V), or methionine (M); the mutation at position 58 is glutamatic acid (E); the mutation at position 71 is leucine (L), isoleucine (I), valine (V), or threonine (T); the mutation at position 82 is alanine (A), phenylalanine (F), serine (S), or threonine (T), and the mutation at position 84 is alanine (A) or cysteine (C), wherein the presence of said mutation indicates that the HIV-1 has an increased likelihood of having reduced susceptibility to treatment with amprenavir, with the proviso that the mutation is not V32I, M46I, M46L, I54L, I54M, or I84V, and wherein the level of susceptibility, mutations, and amino acid position number are compared to the protease sequence of the NL4-3 reference strain.

44. (Canceled)

45. (Currently amended) The method of claim 43–44, wherein the amino acid at position 33 of said protease is detected-F.

46. (Currently amended) The method of claim 43–44, wherein the amino acid at position 48 of said protease is detected-M.

47. (Currently amended) The method of claim 43–44, wherein the amino acid at position 54 of said protease is detected-A.

48. (Currently amended) The method of claim 43–44, wherein the amino acid at position 71 of said protease is detected-L.

49. (Currently amended) The method of claim 43–44, wherein the amino acid at position 82 of said protease is detected A or F.

50. (Currently amended) The method of claim 43–44, wherein the amino acid at position 84 of said protease is detected-A.

51. (Currently amended) The method of claim 43–44, wherein the amino acid at position 43 of said protease is detected–T.

52. (Canceled)

53. (Currently amended) The method of claim 43–52, wherein the amino acid at position 54 of said protease is detected S or T.

54. (Canceled)

55. (Currently amended) The method of claim 43–54, wherein the amino acid at position 58 of said protease is detected–E.

56. (Canceled)

57. (Canceled)

58. (Canceled)

59. (Previously presented) The method of claim 43–58, wherein the amino acid at position 84 of said protease is detected–C.

60. (Currently amended) The method of claim 43, wherein the method comprises detecting the presence or absence of a mutation associated with reduced susceptibility to treatment with amprenavir ~~said protease inhibitor~~ at each one of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16, ~~17, 18 or 19~~ of the amino acid positions.